Amendments to the Claims

The status of the claims is as follows:

1. (Currently Amended) A hybridization assay probe comprising a target binding region ~~from 18 to 35 bases in length~~ that fully hybridizes to a target sequence present in a target nucleic acid derived from a *Cryptosporidium parvum* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection, said target sequence being selected from the group consisting of ~~SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18~~ SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Cryptosporidium wrairi* organism to form a probe:non-target hybrid stable for detection under said conditions.

Claims 2-10 (Canceled)

11. (Previously Presented) The probe of claim 1, wherein said probe contains at least two base regions that hybridize to each other when said probe is not hybridized to said target sequence under said conditions.

12. (Previously Presented) The probe of claim 1, wherein said probe comprises at least one base region that does not stably hybridize to nucleic acid derived from a *Cryptosporidium parvum* organism under said conditions.

13. Canceled

14. (Original) The probe of claim 1 further comprising a detectable label.

15. (Previously Presented) The probe of claim 11 further comprising a group of interacting labels.

16. (Original) The probe of claim 15, wherein said interacting labels include a luminescent label and a quencher label.

17. (Previously Presented) The probe of claim 1, wherein said target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety.

18. (Previously Presented) The probe of claim 1, wherein a pseudo peptide backbone joins at least a portion of the bases of said target binding region.

19. (Previously Presented) The probe of claim 1, wherein said conditions comprise 100 mM succinic acid, 2% (w/v) LLS, 15 mM aldrithiol-2, 1.2 M LiCl, 20 mM EDTA, 3% (v/v) ethyl alcohol (absolute), pH 4.7, and a test sample temperature of about 60°C.

20. (Previously Presented) The probe of claim 1, wherein the base sequence of said target binding region is at least 80% complementary to the base sequence of said target sequence.

21. (Currently Amended) The probe of claim 1, wherein the base sequence of said ~~probe~~ target binding region is ~~at least 80%~~ perfectly complementary to the base sequence of said target sequence.

22. (Currently Amended) The probe of claim 1, wherein the base sequence of said probe is ~~fully~~ perfectly complementary to the base sequence of said target sequence.

23. (Currently Amended) A probe mix comprising said probe of claim 1 and a first helper oligonucleotide ~~from~~ that is at least 18 ~~to 35~~ bases in length ~~that~~ and fully hybridizes to a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41 under stringent conditions.

Claims 24-28 (Canceled)

29. (Currently Amended) The probe mix of claim 23 further comprising a second helper oligonucleotide ~~from~~ that is at least 18 ~~to 35~~ bases in length ~~that~~ and fully hybridizes to a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44 under stringent conditions.

Claims 30-36 (Canceled)

37. (Previously Presented) A method for determining the presence of a *Cryptosporidium parvum* organism in a test sample, said method comprising the steps of:

contacting said test sample with said probe of claim 1 under stringent conditions; and

determining whether a probe:target hybrid has formed as an indication of the presence of a *Cryptosporidium parvum* organism in said test sample.

38. (Currently Amended) The method of claim 37 further comprising providing to said test sample a first amplification oligonucleotide under amplification conditions, said first amplification oligonucleotide comprising a target binding region ~~from~~ that is at least 18 ~~to 40~~ bases

in length ~~that~~ and fully hybridizes to a target sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66 under said amplification conditions, wherein said first amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said first amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

39. (Currently Amended) The method of claim 38 further comprising providing to said test sample a second amplification oligonucleotide under said amplification conditions, said second amplification oligonucleotide comprising a target binding region ~~from~~ that is at least 18 ~~to 40~~ bases in length ~~that~~ and fully hybridizes to a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63 under said amplification conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

40. (Currently Amended) The method of claim 38 further comprising providing to said test sample a second amplification oligonucleotide under amplification conditions, said second amplification oligonucleotide comprising a target binding region ~~from~~ that is at least 18 ~~to 40~~ bases in length ~~that~~ and fully hybridizes to a target sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 under said amplification conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid

containing said target sequence under said amplification conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

Claims 41-49 (Canceled)

50. (Previously Presented) A method for determining the presence of a *Cryptosporidium parvum* organism in a test sample, said method comprising the steps of:

contacting said test sample with said probe of claim 20 under stringent conditions; and

determining whether a probe:target hybrid has formed as an indication of the presence of a *Cryptosporidium parvum* organism in said test sample.

51. (Previously Presented) A method for determining the presence of a *Cryptosporidium parvum* organism in a test sample, said method comprising the steps of:

contacting said test sample with said probe of claim 21 under stringent conditions; and

determining whether a probe:target hybrid has formed as an indication of the presence of a *Cryptosporidium parvum* organism in said test sample.

52. (Previously Presented) A method for determining the presence of a *Cryptosporidium parvum* organism in a test sample, said method comprising the steps of:

contacting said test sample with said probe of claim 22 under stringent conditions; and

determining whether a probe:target hybrid has formed as an indication of the presence of a *Cryptosporidium parvum* organism in said test sample.

53. (Currently Amended) A kit comprising, in packaged combination, first and second oligonucleotides for use in determining the presence of a *Cryptosporidium parvum* organism in a test sample, ~~each of~~ wherein said ~~oligonucleotides~~ first oligonucleotide comprises a target binding region that fully hybridizes to a first target sequence ~~in target nucleic acid derived from a *Cryptosporidium parvum* organism under hybridization conditions, said target binding region of said first oligonucleotide being from 18 to 35 bases in length and said target binding region of said second oligonucleotide being from 18 to 40 bases in length, wherein said target sequence of said first oligonucleotide is~~ selected from the group consisting of ~~SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18~~ SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17 under stringent conditions, wherein said second oligonucleotide comprises a target binding region that is at least 18 bases in length and fully hybridizes to a second ~~said~~ target sequence ~~of said second oligonucleotide is~~ selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66 under amplification conditions, wherein ~~neither of~~ said first ~~and second oligonucleotides comprises~~ oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to ~~said~~ a target nucleic acid containing said first target sequence under said stringent conditions, wherein said second oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said second target sequence under said amplification conditions, wherein said first oligonucleotide does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Cryptosporidium wrairi* organism to form a first oligonucleotide:non-target hybrid stable for detection under said stringent conditions, and wherein said second oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

Claims 54-58 (Canceled)

59. (Currently Amended) The kit of claim 53 further comprising a third oligonucleotide, said third oligonucleotide comprising a target binding region ~~from~~ that is at least 18 ~~to 40~~ bases in length ~~that~~ and fully hybridizes to a third target sequence ~~present in target nucleic acid derived from a *Cryptosporidium parvum* organism under hybridization conditions, said target sequence being~~ selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63 under said amplification conditions, wherein said third oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to ~~said~~ a target nucleic acid containing said third target sequence under said amplification conditions, and wherein said third oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

60. (Currently Amended) The kit of claim 53 further comprising a third oligonucleotide, said third oligonucleotide comprising a target binding region from that is at least 18 ~~to 40~~ bases in length ~~that~~ and fully hybridizes to a third target sequence present ~~in target nucleic acid derived from a *Cryptosporidium parvum* organism under hybridization conditions, said target sequence being~~ selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 under said amplification conditions, wherein said third oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to ~~said~~ a target nucleic acid containing said third target sequence under said amplification conditions, and wherein said third oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

Claims 61-83 (Canceled)

84. (Currently Amended) A kit comprising, in packaged combination, first and second oligonucleotides for use in determining the presence of a *Cryptosporidium parvum* organism

in a test sample, ~~each of~~ wherein said ~~oligonucleotides comprising~~ first oligonucleotide comprises a target binding region ~~from 18 to 35 bases in length~~ that fully hybridizes to a first target sequence ~~present in target nucleic acid derived from a *Cryptosporidium parvum* organism under stringent conditions, wherein said target sequence of said first oligonucleotide is~~ selected from the group consisting of ~~SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18~~ SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 and SEQ ID NO:17 under stringent conditions, wherein ~~said target sequence of~~ said second oligonucleotide is at least 18 bases in length and fully hybridizes to a second target sequence ~~is~~ selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41 under said conditions, wherein ~~neither of~~ said first ~~and second oligonucleotides comprises~~ oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to ~~said~~ a target nucleic acid containing said first target sequence under said conditions, and wherein said first oligonucleotide does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Cryptosporidium wrairi* organism to form a ~~probe:non-target~~ first oligonucleotide:non-target hybrid stable for detection under said conditions.

Claims 85-93 (Canceled)

94. (Currently Amended) A probe mix comprising said probe of claim 20 and a first helper oligonucleotide ~~up to 35~~ that is at least 18 bases in length and ~~having a base sequence that is at least 80%~~ fully complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41, wherein said first helper oligonucleotide hybridizes to said target sequence under stringent conditions.

95. (Currently Amended) The probe mix of claim 94 further comprising a second helper oligonucleotide ~~up to 35~~ that is at least 18 bases in length and ~~having a base sequence that is~~

~~at least 80%~~ fully complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44, wherein said second helper oligonucleotide hybridizes to said target sequence under stringent conditions.

96. (Currently Amended) A probe mix comprising said probe of claim 21 and a first helper oligonucleotide, wherein the base sequence of said first helper oligonucleotide is ~~at least 80%~~ perfectly complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41~~, wherein said first helper oligonucleotide hybridizes to said target sequence under stringent conditions~~.

97. (Currently Amended) The probe mix of claim 96 further comprising a second helper oligonucleotide, wherein the base sequence of said second helper oligonucleotide is ~~at least 80%~~ perfectly complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44~~, wherein said second helper oligonucleotide hybridizes to said target sequence under stringent conditions~~.

98. (Currently Amended) A probe mix comprising said probe of claim 22 and a first helper oligonucleotide, wherein the base sequence of said first helper oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41.

99. (Currently Amended) The probe mix of claim 98 further comprising a second helper oligonucleotide, wherein the base sequence of said second helper oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44.

Claims 100-113 (Canceled)

114. (Currently Amended) The method of claim 50 further comprising providing to said test sample a first amplification oligonucleotide under amplification conditions, said first amplification oligonucleotide comprising a target binding region that is at least ~~from~~ 18 ~~to 40~~ bases in length ~~that~~ and fully hybridizes to a target sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66 under said amplification conditions, wherein the base sequence of said target binding region is at least 80% complementary to the base sequence of said target sequence, wherein said first amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said first amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

115. (Currently Amended) The method of claim 114 further comprising providing to said test sample a second amplification oligonucleotide under said amplification conditions, said second amplification oligonucleotide comprising a target binding region that is at least ~~from~~ 18 ~~to 40~~ bases in length ~~that~~ and fully hybridizes to a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63 under said amplification conditions, wherein the base sequence of said target binding region is at least 80% complementary to the base sequence of said target sequence, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

116. (Currently Amended) The method of claim 114 further comprising providing to said test sample a second amplification oligonucleotide under said amplification conditions, said second amplification oligonucleotide comprising a target binding region that is at least ~~from~~ 18 ~~to~~ ~~40~~ bases in length ~~that~~ and fully hybridizes to a target sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 under said amplification conditions, wherein the base sequence of said target binding region is at least 80% complementary to the base sequence of said target sequence, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

Claims 117-120 (Canceled)

121. (Currently Amended) The method of claim 51 further comprising providing to said test sample a first amplification oligonucleotide comprising a target binding region under amplification conditions, wherein the base sequence of said target binding region is ~~at least 80%~~ perfectly complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66, ~~wherein said target binding region hybridizes to said target sequence under said amplification conditions;~~ wherein said first amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said first amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

122. (Currently Amended) The method of claim 121 further comprising providing to said test sample a second amplification oligonucleotide comprising a target binding region under amplification conditions, wherein the base sequence of said target binding ~~regon~~ region is ~~at least~~ ~~80%~~ perfectly complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63, ~~wherein said target binding region hybridizes to said target sequence under said amplification conditions,~~ wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

123. (Currently Amended) The method of claim 121 further comprising providing to said test sample a second amplification oligonucleotide comprising a target binding region under amplification ~~conditioins~~ conditions, wherein the base sequence of said target binding region is ~~at least 80%~~ perfectly complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64, ~~wherein said target binding region hybridizes to said target sequence under said amplification conditions,~~ wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

124. (Currently Amended) The method of claim 52 further comprising providing to said test sample a first amplification oligonucleotide comprising a target binding region under

amplification conditions, wherein the base sequence of said target binding region is ~~fully~~ perfectly complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66, ~~wherein said target binding region hybridizes to said target sequence under said amplification conditions;~~ wherein said first amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said first amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

125. (Currently Amended) The method of claim 124 further comprising providing to said test sample a second amplification oligonucleotide comprising a target binding region under amplification conditions, wherein the base sequence of said target binding region is ~~fully~~ perfectly complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63, ~~wherein said target binding region hybridizes to said target sequence under said amplification conditions;~~ wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

126. (Currently Amended) The method of claim 124 further comprising providing to said test sample a second amplification oligonucleotide comprising a target binding region under amplification conditions, wherein the base sequence of said target binding region is ~~fully~~ perfectly complementary to the base sequence of a target sequence selected from the group consisting of SEQ

ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64, ~~wherein said target binding region hybridizes to said target sequence under said amplification conditions,~~ wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

Claims 127-132 (Canceled)

133. (Currently Amended) The kit of claim 53, wherein the base sequence of said target binding region of ~~each~~ said first oligonucleotide is at least 80% complementary to the base sequence of said first target sequence, and wherein the base sequence of said target binding region of said second oligonucleotide is at least 80% complementary to the base sequence of said second target sequence.

134. (Currently Amended) The kit of claim 53, wherein the base sequence of said target binding region of ~~each~~ said first oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said first target sequence, and wherein the base sequence of said target binding region of said second oligonucleotide is perfectly complementary to the base sequence of said second target sequence.

135. (Currently Amended) The kit of claim 53, wherein the base sequence of ~~each~~ said first oligonucleotide is at least 80% complementary to the base sequence of said first target sequence, and wherein the base sequence of said second oligonucleotide is at least 80% complementary to the base sequence of said second target sequence.

136. (Currently Amended) The kit of claim 53, wherein the base sequence of ~~each~~ said first oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said first target sequence, and wherein the base sequence of said second oligonucleotide is perfectly complementary to the base sequence of said second target sequence.

137. (Currently Amended) The kit of claim 59, wherein the base sequence of said target binding region of ~~each~~ said first oligonucleotide is at least 80% complementary to the base sequence of said first target sequence, wherein the base sequence of said target binding region of said second oligonucleotide is at least 80% complementary to the base sequence of said second target sequence, and wherein the base sequence of said target binding region of said third oligonucleotide is at least 80% complementary to the base sequence of said third target sequence.

138. (Currently Amended) The kit of claim 59, wherein the base sequence of said target binding region of ~~each~~ said first oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said first target sequence, wherein the base sequence of said target binding region of said second oligonucleotide is perfectly complementary to the base sequence of said second target sequence, and wherein the base sequence of said target binding region of said third oligonucleotide is perfectly complementary to the base sequence of said third target sequence.

139. (Currently Amended) The kit of claim 59, wherein the base sequence of ~~each~~ said first oligonucleotide is at least 80% complementary to the base sequence of said first target sequence, wherein the base sequence of said second oligonucleotide is at least 80% complementary to the base sequence of said second target sequence, and wherein the base sequence of said third oligonucleotide is at least 80% complementary to the base sequence of said third target sequence.

140. (Currently Amended) The kit of claim 59, wherein the base sequence of ~~each~~ said first oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said first target sequence, wherein the base sequence of said second oligonucleotide is perfectly complementary to the base sequence of said second target sequence, and wherein the base sequence of said third oligonucleotide is perfectly complementary to the base sequence of said third target sequence.

141. (Currently Amended) The kit of claim 60, wherein the base sequence of said target binding region of ~~each~~ said first oligonucleotide is at least 80% complementary to the base sequence of said first target sequence, wherein the base sequence of said target binding region of said second oligonucleotide is at least 80% complementary to the base sequence of said second target sequence, and wherein the base sequence of said target binding region of said third oligonucleotide is at least 80% complementary to the base sequence of said third target sequence.

142. (Currently Amended) The kit of claim 60, wherein the base sequence of said target binding region of ~~each~~ said first oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said first target sequence, wherein the base sequence of said target binding region of said second oligonucleotide is perfectly complementary to the base sequence of said second target sequence, and wherein the base sequence of said target binding region of said third oligonucleotide is perfectly complementary to the base sequence of said third target sequence.

143. (Currently Amended) The kit of claim 60, wherein the base sequence of ~~each~~ said first oligonucleotide is at least 80% complementary to the base sequence of said first target sequence, wherein the base sequence of said second oligonucleotide is at least 80% complementary to the base sequence of said second target sequence, and wherein the base sequence of said third oligonucleotide is at least 80% complementary to the base sequence of said third target sequence.

144. (Currently Amended) The kit of claim 60, wherein the base sequence of ~~each~~ said first oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said first target sequence, wherein the base sequence of said second oligonucleotide is perfectly complementary to the base sequence of said second target sequence, and wherein the base sequence of said third oligonucleotide is perfectly complementary to the base sequence of said third target sequence.

Claims 145-150 (Canceled)

151. (Currently Amended) The kit of claim 84, wherein the base sequence of said target binding region of ~~each~~ said first oligonucleotide is at least 80% complementary to the base sequence of said first target sequence, and wherein the base sequence of said second oligonucleotide is at least 80% complementary to the base sequence of said second target sequence.

152. (Currently Amended) The kit of claim 84, wherein the base sequence of said target binding region of ~~each~~ said first oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said first target sequence, and wherein the base sequence of said second oligonucleotide is perfectly complementary to the base sequence of said second target sequence.

153. (Currently Amended) The kit of claim 84, wherein the base sequence of ~~each~~ said first oligonucleotide is at least 80% complementary to the base sequence of said first target sequence, and wherein the base sequence of said second oligonucleotide is at least 80% complementary to the base sequence of said second target sequence.

154. (Currently Amended) The kit of claim 84, wherein the base sequence of ~~each~~ said first oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said first target

sequence, and wherein the base sequence of said second oligonucleotide is perfectly complementary to the base sequence of said second target sequence.

155. (Currently Amended) The kit of claim 84 further comprising a third oligonucleotide ~~from~~ that is at least 18 ~~to 35~~ bases in length that and fully hybridizes to a third target sequence present in ~~target~~ nucleic acid derived from a *Cryptosporidium parvum* organism under stringent conditions, said third target sequence being selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44.

156. (Currently Amended) The kit of claim 155, wherein ~~each~~ the base sequence of said target binding region of said first oligonucleotide ~~has a base region that~~ is at least 80% complementary to the base sequence of said first target sequence, wherein the base sequence of said second oligonucleotide is at least 80% complementary to the base sequence of said second target sequence, and wherein the base sequence of said third oligonucleotide is at least 80% complementary to the base sequence of said third target sequence.

157. (Currently Amended) The kit of claim 155, wherein ~~each~~ the base sequence of said target binding region of said first oligonucleotide ~~has a base region that~~ is ~~fully~~ perfectly complementary to the base sequence of said first target sequence, wherein the base sequence of said second oligonucleotide is perfectly complementary to the base sequence of said second target sequence, and wherein the base sequence of said third oligonucleotide is perfectly complementary to the base sequence of said third target sequence.

158. (Currently Amended) The kit of claim 155, wherein the base sequence of ~~each~~ said first oligonucleotide is at least 80% complementary to the base sequence of said first target sequence, wherein the base sequence of said second oligonucleotide is at least 80% complementary

to the base of said second target sequence, and wherein the base sequence of said third oligonucleotide is at least 80% complementary to the base sequence of said third target sequence..

159. (Currently Amended) The kit of claim 155, wherein the base sequence of ~~each~~ said first oligonucleotide is ~~fully~~ perfectly complementary to the base sequence of said first target sequence, wherein the base sequence of said second oligonucleotide is perfectly complementary to the base sequence of said second target sequence, and wherein the base sequence of said third oligonucleotide is perfectly complementary to the base sequence of said third target sequence.

160. (New) The probe of claim 1, wherein said target binding region of said probe is at least 18 bases in length.

161. (New) The method of claim 37, wherein said target binding region of said probe is at least 18 bases in length.

162. (New) The kit of claim 53, wherein said target binding region of said first oligonucleotide is at least 18 bases in length.

163. (New) The kit of claim 84, wherein said target binding region of said first oligonucleotide is at least 18 bases in length.